

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Gaugler, Béatrice; Van den Eynde, Benoît;
van der Bruggen, Pierre; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/037,230
(B) FILING DATE: 26-MARCH-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991
- (ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: 23-SEPTEMBER-1991
- (x) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/728,838
(b) FILING DATE: 9-JULY-1991
- (xi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/705,702
(B) FILING DATE: 23-MAY-1991
- (xii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 253.5
- (xiii) TELECOMMUNICATION INFORMATION:
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- (2) INFORMATION FOR SEQUENCE ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAGACG CTAGATGTGT GAAGATCCTG 60
 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGTCA AGTTCCGCCT ACAGCTCTAG 180
 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

- (2) INFORMATION FOR SEQUENCE ID NO: 2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
 5 10 15
 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
 20 25 30
 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
 35 40 45
 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
 50 55 60
 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
 65 70 75 80
 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
 85 90 95
 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336
 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
 100 105 110
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
 115 120 125
 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
 130 135 140
 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
 145 150 155 160
 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
 165 170 175
 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
 180 185 190
 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG 624
 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu
 195 200 210
 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
 Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
 220 225 230 235

675

TAG

- (2) INFORMATION FOR SEQUENCE ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228

D

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1365 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTGTGGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGCTG TGCTGAGTTT AGLAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
 TAG 1137
 GCATGCAGTT GCAAAGCCCA GAGGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
 TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGATACCT 1337
 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4698 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAGACG CTAGATGTGT 50
 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T 916
 GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA 966
 CTCTTGCCCA CATCTGTAGT AAGACCAACA TTTTGGTTGG GGGTCATTGC 1016
 TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC 1066
 CCCCACCTCT TGCTCCGCTC TCTTTCTTTT TCCCACCTTG CCTCTGGAGC 1116
 TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGTCTC CTTGCTCCCC 1166
 TCCCCCTCGG CTCACCTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCTCT 1216
 TTCAGGCTTC CCCATTGCT CCTCTCCCGA AACCTCCCTT TCCCTGTTC 1266
 CCTTTTCCGC CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT 1316
 TCACCAGCTT TGCTCTCCCT GCTCCCTCC CCTTTTGA CCTTTTCTTT 1366
 TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT 1416
 CTACCTGCTT CCTCCCCCT TGCTGCTCCC TCCCTATTG CATTTTCGGG 1466
 TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT 1516
 CCTCCCTCCC CCTCCCCAGG CCTTTTCTTT TTTTCTTTT TTTTCTTTT 1566
 TTGGTTTTTC GAGACAGGTT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC 1616
 TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG 1666
 CCTCCCAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG 1716
 GCCTTTCTTT TTTCTCTCT CTGCTCTCCC TAATCCCTTT TCTGCATGTT 1766
 AACTCCCTTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCTCCCTGT 1816
 TTCCCTTCCG GCACCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC 1866
 CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CTTGCTTTCT 1916
 GCCCGGTTCC CCTTTTGTG GCCTTTCTCT CTGCTCCCC TCCACCTTCC 1966
 AGCTCACCTT TTTGTTGTT TTGTTGTTG GTTGTGTTG TTGCTTTT 2016
 TTTTCTTTT GCACCTTGT TTCCAAGATC CCCCCTCCCC TCCGGCTTCC 2066
 CCTCTGTGTG CCTTCTCTGT TCCCTCCCC TCGCTGGCTC CCCCCTCCTT 2116
 TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT 2166
 CTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT 2216
 CCTGACCCTG CTCCCCCTCC CCTCCCAGCT CCCCCTCTT TTCCCACCTC 2266
 CCTTTCTCCA GCCTGTACAC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT 2316
 TCCTGCTTCC TTTACCCCTT CCTCTCCCT ACTCTCTCC CTGCCTGCTG 2366
 GACTTCTCT CCAGCCGCCC AGTTCCCTGC AGTCCCTGG TCTTTCTGTC 2416
 CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTC ACTCTCCCTT 2466
 ATGTGTCTCT CTTCTATCT ATCCCTTCTT TTCTGTCCCC TCTCCTCTGT 2516
 CCATCACCTC TCTCCTCCCT TCCCTTCTCT CTCTCTTCCA TTTTCTTCCA 2566
 CCTGCTTCTT TACCCTGCCT CTCCCATTC CCTCTTACCT TTATGCCCAT 2616
 TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC 2666

ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC 2716
 TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCTATG CCCTCTACTC 2766
 TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC 2816
 CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC 2866
 ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCCAA ATCAGCAGGA 2916
 AAGGCTGGAT GAAATAAGG CCAAGTTCTG AGGACAGCTG GAATCTAGCC 2966
 AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT 3016
 CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG 3066
 CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA 3116
 GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG 3166
 TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA 3216
 TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA 3266
 GGCTAAAGAT ACTTGAACCC ATAGAAGCGT TGTAAATAA CTGCTTTCTT 3316
 TTGCTAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG 3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT 3396
 AGG ATG ATT TAT TTC CAC GAC CCT AAT TTC CTG GTG TCT 3438
 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA 3480
 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA 3522
 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC 3564
 TTC TCA CCT TAG 3576
 GCATGCAGGT ACTGGCTTCA CTAAACCAACC ATTCTTAACA TATGCCTGTA 3626
 GCTAAGAGCA TCTTTTTTAAA AATATTTATT GGTAAACTAA ACAATTGTTA 3676
 TCTTTTTTACA TTAATAAGTA TTAATTAAAT CCAGTATACA GTTTTAAGAA 3726
 CCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT 3776
 GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA 3826
 GACCAGTAAA AGATCATGCA GTGAATGTG GCCATGGAAA TCGCATATTG 3876
 TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT 3926
 TTCAAGAAAG ATCACACGCC ATGTTTACA TGCAATTAT TATTTTGTCTG 3976
 TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT 4026
 CTTAAATTT CCTTCATCTT TATTTTTCCT TAACTTTAGT TTTTTCACT 4076
 TAGAATTCAA TTCAAATTCT TATTTCAATC TTAATTTTAA GATTTCTTAA 4126
 AATGTTTTT AAAAAAATG CAATCTCAT TTTTAAGAGA TGAAAGCAGA 4176
 GTAACGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226
 GTTCTGTCT CTGAGAAGCA GTCAGAGAGA ATGGAANAACC AGGCCCTTGC 4276
 CAGTAGGTTA GTGAGGTGA TATGATCAGA TTATGGACAC TCTCCAAATC 4326
 ATAAATACTC TAACAGCTAA GATCTCTGA GGGAAACACA ACAGGGAAAT 4376
 ATTTTAGTTT CTCCTTGAGA AACAAAGACA AGACATAAAA TTGGCAAGAA 4426
 AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTTCTTCTAC 4476
 AGTTGCAAG CCCAGAGAA AGAATGGAC AGCGGAGAA GTGGTTGTTT 4526
 TTTTTTCCCC TTCAATTAAT TTCTAGTTT TAGTAATCCA GAAATTTGA 4576
 TTTTGTCTA AAGTTCAATG TGCAAGATG TCACCAACAG ACTTCTGACT 4626
 GCATGCTGAA CTTTCATATG ATACATAGGA TTACACTGT ACCTGTAAAA 4676
 AATAAAGTT TGACTTGCAT AC 4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
5

21

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2418 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50
 GGGGTTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100
 TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150
 GGCCCGTGGA TTCTCTTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAGGACACAT AGGACTCCAC AGAGTCTGSC CTCACCTCCC TACTGTCACT 350
 CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC 400
 TTCTCTCTTC AGGTTTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC 450
 CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500
 TTAGAGTCTC CAAGGTTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT 550
 CTCTCCCCAG GCCTGTGGGT CTTTATTGCC CAGCTCCTGC CCACACTCCT 600
 GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650
 ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAAGAGG CCTGGGCGCTG 700
 GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC 750
 CCTGGAGGAG GTGCCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800
 AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850
 CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900
 TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950
 TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000
 GCAGAAATGC TGGAGAGTGT CATCAAAAT TACAAGCACT GTTTTCCTGA 1050
 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGAGC 1100
 TGAAGGAAGC AGACCCCAACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
 AGGCTTCTCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGGGCCATG 1250
 CTCTTGAGGA GGAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
 GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
 TTTGGTGCA GAAAGTACC TGGAGTACCG CAGGTGCCCG ACAGTGATCC 1400
 CGCACGCTAT GAGTTCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
 TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
 CTGAGCATGA GTTGCAAGCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650
 CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCTCAGT AGTAGGTTTC 1700
 TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750
 TCAATATGTT TTTTAAAGG GATGGTTGAA TGAATTCAG CATCCAAGTT 1800
 TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA 1850
 GTCTTGTTGT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900
 ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA 1950
 AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC 2000
 CTTATACCTC AGTCTATTCT GTAAATTTT TAAAGATATA TGCATACCTG 2050
 GATTTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
 AATTCCTTCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150
 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
 AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
 GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG 2350
 GGCATTTTGG GCTTTGGGAA ACTGCASTTC CTCTGGGGG AGCTGATTGT 2400
 AATGATCTTG GGTGGATCC 2418

- (2) INFORMATION FOR SEQUENCE ID NO: 8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5724 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-1 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50
 TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCAGCC CAAGCCAGGC 100
 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG 150
 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTT 200
 CCGTCTGAGG GCGGCTTGA GATCGGTGGA TCGAGGAGG CCCAGCTCTG 250
 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
 AGATAGAGGA CCCCCAATAA TCCCTTCATG CCAGTCCCTG ACCATCTGGT 350
 GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400
 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
 ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCTATT CCAACCCCCA 600
 CCCCACATCC CCCCACCCAT CCCCCTCAACC TGATGCCCAT CCGCCAGCC 650
 ATTCCACCCT CACCCCCACC CCCCACCCCA CGCCCCTCC CACCCCCACC 700
 CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750
 GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG 800
 AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850
 AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCAAATA 900
 GAGAGCCCCA AATATTCCAG CCCCCTCCTT GCTGCCAGCC CTGGCCACC 950
 CGCGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG 1000
 CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC 1050
 TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA 1100
 GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC 1150
 ACTCCAATCC CCACTCCAC CCCATTGCA TTCCCATTC CCACCCAACC 1200
 CCCATCTCCT CAGCTACACC TCCACCCCA TCCCTACTCC TACTCCGTCA 1250
 CCTGACCACC ACCCTCCAGC CCCAGCACA GCCCAACCC TTCTGCCACC 1300
 TCACCCCTCA TCCCCCAAC CCCCCTCA TCTCTCTCAT GTGCCCCACT 1350
 CCCATCGCCT CCCCCATTCT GGCAGATCC GGTGTGCCCT TGCTCTCAAC 1400
 CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC 1450
 AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGG GCGGCTTGAG 1500
 ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG 1550
 CTGAGGGAGG ACTGAGGAG CACACACCCC AGGTAGATGG CCCCCAAATG 1600
 ATCCAGTACC ACCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT 1650
 GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG 1700
 GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGTT GGTGAGGAGA 1750
 GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCGGCAT TAGGGTCAGG 1800
 ACCCTGGGAG GGAAGTGAAG GTTCCCCACC CACACCTGTC TCCTCATCTC 1850
 CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCAACCTCA 1900
 TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC 1950
 CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG 2000
 GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA 2050
 GGGAGGCCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG 2100
 ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA 2150
 TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA 2200
 GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCTT 2250
 GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT 2300
 TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC 2350
 AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG 2400
 AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG 2450
 CTGTCCCTTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG 2500
 TTCCATTCTC ACTGTACCA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG 2550
 ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGAATTGGG 2600
 GGTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT GAGACAGACA 2650
 AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTGAGC CCTGGACACC 2700

TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTITCCAGA TCTGGGGCAG 2750
 GTGAGGACCT CATTCTCAGA GGGTGA CTCA GGTCAACGTA GGGACCCCA 2800
 TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG 2850
 GAACATGAGG GAGGACTGAG GGTACCCAG GACCAGAACTA CTGAGGGGAGA 2900
 CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCAGAG AGCATGGGCT 2950
 GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG 3000
 ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC 3050
 GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC 3150
 CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC 3200
 AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCCTCT GTCCCTCCAT 3250
 TCCTTATCAT GGTATGTGAAC TCTTGATTTG GATTTCTCAG ACCAGCAAAA 3300
 GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TCGGTGAGAA 3350
 CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GATCCAGCC 3400
 CACCCTCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GSTCTGCACC 3450
 CTGAGGGCCC TGCGATTCCCT CTTCCTGGAG CTCCAGGAAC CAGGCAGTGA 3500
 GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG 3550
 GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC 3600
 TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG 3650
 TCAGTCTCTG AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT 3700
 CTCCTTCTCT CTTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG 3750
 ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC 3800
 CTTTGTTAGA GTCTCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC 3850
 TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCAGCT CCTGCCACA 3900
 CTCCTGCCTG CTGCCCTGAC GAGAGTCATC 3930
 ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA 3972
 GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG 4014
 CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC 4056
 CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG 4098
 AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC 4140
 ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA 4182
 GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC 4224
 CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT 4266
 CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA 4308
 GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT 4350
 CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC 4392
 TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC 4434
 TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG 4476
 CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA 4518
 ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT 4560
 GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT 4602
 GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG 4644
 CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC 4686
 AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG 4728
 GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA 4761
 AAGTCTTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC 4800
 GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG 4850
 GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGAAGTGGCC 4900
 AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA 4950
 TGAGGCCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG 5000
 GTTCTGTGTT TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA 5050
 ATTGTTCAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC 5100
 AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG 5150
 TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTGTGAA 5200
 TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAATGT GAAAAATGAG 5250
 CAGTAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT 5300
 CTTGCCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT 5350
 ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA 5400
 TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA 5450
 TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TTGAGATGCT AAGGTAAGCC 5500
 AGACTCATAC CCACCCATAG GGTCTGAGAG TCTAGGAGCT GCAGTCACGT 5550
 AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG 5600
 GGTGAGGGTG TGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA 5650
 GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGAGCTG 5700
 ATTGTAATGA TCTTGGGTGG ATCC 5724

- (2) INFORMATION FOR SEQUENCE ID NO: 9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4157 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-2 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA TCCCCATCCG GGCAGAATCC GGTTCACCC TTGCCGTGAA 50
 CCCAGGGAAG TCACGGGGCCC GGATGTGACG CCACTGACTT GCACATTGGA 100
 GGTGAGAGGA CAGCGAGATT CTCGCCCTGA GCAACGGCCT GACGTCGGCG 150
 GAGGGAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG 200
 AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC 250
 GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAAGGGAA GACTTCTCAG 300
 GCTCAGTCCG CACCACCTCA CCCC GCCCACC CCCC GCCGCT TTAACCGCAG 350
 GGAACCTCTG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAG 400
 TGCTCAGGGC CCAGACTCAG CCAGGAATCA AGGTCAGGAC CCAAGAGGG 450
 GACTGAGGGC AACCCACCCC CTACCCTCAC TACCAATCCC ATCCCCAAC 500
 ACCAACCCCA CCCCCATCCC TCAAACACCA ACCCCACCCC CAAACCCCAT 550
 TCCCATCTCC TCCCCACCA CCATCCTGGC AGAATCCGGC TTGCCCCCTG 600
 CAATCAACCC ACGGAAGCTC CGGGAATGCG GGCCAGCAC GCGGATCCTG 650
 ACGTTCACAT GTACGGCTAA GGGAGGGAG GGGTTGGGTC TCGTGAGTAT 700
 GGCCTTTGGG ATGCAGAGGA AGGGCCGAGG CCTCCTGGA GACAGTGGAG 750
 TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCTGTG 800
 TCAAACCTGAG CCACCTTTTC ATTGAGCCGA GGAATCCTA GGGATGCAGA 850
 CCCACTTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAA GGGGAGGAAG 900
 AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG 950
 GCTGGGGGAT CTGGGGCACA GTGGCCGAT GTGCCCGTG CTCATTGCAC 1000
 CTTGAGGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGCG TGGGACTTCA 1050
 GGTCAGCAGA GGGAGGAATC CCAGGATCTG CCGGACCCAA GGTGTGCCCC 1100
 CTTGATGAGG ACTCCCCATA CCCCCGGCCC AGAAAGAAAG GATGCCACAG 1150
 AGTCTGGAAG TAAATTGTTC TTAGCTCTGG GGAACCTGA TCAGGGATGG 1200
 CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCCCT 1250
 CAGGGAGATA AGGTGTTGGT GTAAAGAGGA GCTGTCTGCT CATTTCAGGG 1300
 GGTTCCCCCT TGAGAAAGGG CAGTCCCTGG CAGGAGTAA GATGAGTAAC 1350
 CCACAGGAGG CCATCATAAC GTTCACCCTA GAACCAAGG GGTGAGCCCT 1400
 GGACAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTTC 1450
 CAGATCTCAG GGAGTTGATG ACCTTGTTT CAGAAGGTGA CTCAGTCAAC 1500
 ACAGGGGGCCC CTCTGGTCGA CAGATGCAGT GGTCTAGGA TCTGCCAAGC 1550
 ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCTT GGGCCAGAAT 1600
 GCAGCAAGGG GGCCCCATAG AAATCTGCCC TGCCCTGCG GTTACTTCAG 1650
 AGACCCTGGG CAGGGCTGTC AGCTGAAGTC CCTCCATTAT CTGGGATCCT 1700
 TGATGTCAGG GAAGGGGAGG CCTTGGTCTG AAGGGGCTGG AGTCAGGTCA 1750
 GTAGAGGGAG GGTCTCAGGC CCTGCCAGGA GTGGACGTGA GGACCAAGCG 1800
 GACTCGTCAC CCAGGACACC TGGACTCCAA TGAATTTGAC ATCTCTCGTT 1850
 GTCCTTCGCG GAGGACCTGG TCACGTATGG CCAGATGTGG GTCCCTCTA 1900
 TCTCCTTCTG TACCATATCA GGGATGTGAG TTCTTGACAT GAGAGATTCT 1950
 CAAGCCAGCA AAAGGGTGGG ATTAGGCCCT ACAAGGAGAA AGGTGAGGGC 2000
 CCTGAGTGAG CACAGAGGGG ACCCTCCACC CAAGTAGAGT GGGGACCTCA 2050
 CGGAGTCTGG CCAACCCTGC TGAGACTTCT GGAATCCGT GGCTGTGCTT 2100
 GCAGTCTGCA CACTGAAGGC CCGTGCATTC CTCTCCAGG AATCAGGAGC 2150
 TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTCA 2200
 AGAGCAGAGG GGACGCAGAC AGTGCCAACA CTGAAGGTTT GCCTGGAATG 2250
 CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCCTG 2300
 GCCTCACCCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG 2350
 CTGTACCCTG AGGTGCCCTC CCACTTCCTC CTTGAGGTTT TGAGGGGGAC 2400
 AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAGAAGAT 2450
 CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTTCAGTTC AGTTCTCACC 2500
 TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCAATTG 2550
 CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC 2597
 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 2639
 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 2681
 CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT 2723

TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC 2765
 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807
 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849
 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT 2891
 CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933
 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017
 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059
 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101
 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143
 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3185
 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227
 ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3269
 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC 3311
 TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG 3353
 GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT 3395
 GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA 3437
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT 3479
 GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT 3521
 TTG AGA GAG GGA GAA GAG TGA 3542
 GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 3592
 GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642
 GGCCCATTTCC TGCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692
 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742
 TTGTTCAAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
 TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892
 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942
 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992
 TGCTTTATAC CTCAGTCTAT TATGTAAAT TAAAAATATG TGTATGTTTT 4042
 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092
 TCACTGGCTC ATTCTTTTAC CATTCACCTCA GCATCTGCTC TGTGGAAGGC 4142
 CCTGCTAGTA GTGGG 4157

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-21 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC 50
 AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT 100
 CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG 150
 GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG 200
 ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG 250
 CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC 300
 AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA 350
 CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT 400
 CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT 450
 GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA 500
 CCCCACCCCC ATCCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA 550
 ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG 600
 GAGCTTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA 650
 GCACGCGGAT CC 662

- (2) INFORMATION FOR SEQUENCE ID NO: 11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (ix) FEATURE:
 (A) NAME/KEY: cDNA MAGE-3
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGSCTCGGTG AGGAGGCAAG GTTCTGAGGG 50
 GACAGGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100
 AGATCTGCCA GTGGGTCTCC ATTGCCACG TCCTGCCAC ACTCCCGCCT 150
 GTTGCCCTGA CCAGATCAT C 171
 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213
 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255
 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297
 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
 CCC AAG GCA GGC CTC CTG ATA ATC CTC GGC ATA ATC GCA 801
 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
 TTG AGA GAG GGG GAA GAG TGA 1116
 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1216
 GGCCCATTTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
 TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1316
 TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG 1416
 TAAGAGTCTT GtctTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
 ATTCTTGCC TGTACCTCAA TCTATCTGT AAAATTAAC AAATATGCAA 1616
 ACCAGGATT CCTTGACTTC TTG 1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 base pairs

(B) TYPE: nucleic acid


(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:



GGATCCTCCA	CCCCAGTAGA	GTGGGGACCT	CACAGAGTCT	GGCCAACCCT	50
CCTGACAGTT	CTGGGAATCC	GTGGCTGCGT	TTGCTGTCTG	CACATTGGGG	100
GCCCCGTGGAT	TCCTCTCCCA	GGAATCAGGA	GCTCCAGGAA	CAAGGCAGTG	150
AGGACTTGGT	CTGAGGCAGT	GTCCTCAGGT	CACAGAGTAG	AGGGGgCTCA	200
GATAGTGCCA	ACGGTGAAGG	TTTGCCTTGG	ATTCAAACCA	AGGGCCCCAC	250
CTGCCCCAGA	ACACATGGAC	TCCAGAGCGC	CTGGCCTCAC	CCTCAATACT	300
TTCAGTCCTG	CAGCCTCAGC	ATGCGCTGGC	CGGATGTACC	CTGAGGTGCC	350
CTCTCACTTC	CTCCTTCAGG	TTCTGAGGGG	ACAGGCTGAC	CTGGAGGACC	400
AGAGGCCCCC	GGAGGAGCAC	TGAAGGAGAA	GATCTGTAAG	TAAGCCTTTG	450
TTAGAGCCTC	CAAGGTTCCA	TTCAGTACTC	AGCTGAGGTC	TCTCACATGC	500
TCCCTCTCTC	CCCAGGCCAG	TGGGTCTCCA	TTGCCAGCT	CCTGCCCCACA	550
CTCCCGCCTG	TTGCCCTGAC	CAGAGTCATC			580
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	622
GGC CTT GAG	GCC CGA GGA	GAg GCC CTG	GGC CTG GTG	GGT GCG	664
CAG GCT CCT	GCT ACT GAG	GAG CAg GAG	GCT GCC TCC	TCC TCT	706
TCT AGT GTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	748
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	790
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	832
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	874
CCT GAC CTG	GAG TCT GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	916
GTG GCC AAG	TTG GTT CAT	TTT CTG CTC			943

- (2) INFORMATION FOR SEQUENCE ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2531 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-4 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350
 CCTGCAGAAAT CGACCTCTGC TGGCCGGGCTA TACCCTGAGG TGCTCTCTCA 400
 CTTCTCTCCT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500
 TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTGG 600
 CCTGTGCCCC TGACCAGAGT CATC 624
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA 708
 CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC 750
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002
 GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC 1044
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128
 GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254
 GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG 1296
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548
 GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA 1578
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678
 CATTCCTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT 1728
 TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT 1778
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCATTTT TGTGAATTTG 1928
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978
 GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA 2028
 GTCTATTCTG TAAATTTTAA AAATATATAT GCATACCTGG ATTTCTTGG 2078
 CTTCTGTAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA 2128
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAGGGCCC 2178
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228
 GGGTATTAAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328
 GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378
 AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC 2428
 AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC 2478

TCIGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT
GGG

2528
2531



(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2531 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-41 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTGTCTCT AGGTTACAGA GCAGAGGATG CACAGGCTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350
 CCTGCAGAAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400
 CTTCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500
 TAGAGCCTCT AAGATTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTCTG 600
 CCTGCTGCCC TGAGCAGAGT CATC 624
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG 708
 CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC 750
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GGG CCA AGC ACC 918
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002
 GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC 1044
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128
 GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254
 GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG 1296
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548
 GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA 1578
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678
 CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTCTTCA GTAGTGGGTT 1728
 TCTATTTTGT TGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT 1778
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTCTATTT TGTGAATTTG 1928
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978
 GAAATAGGTG AGATAAATTA AAAGATACTT AATTCACCGC TTATGCCTCA 2028
 GTCTATTCTG TAAATTTTAA AAATATATAT GCATACCTGG ATTTCCCTTG 2078
 CTTCTGTAAT GTAAGAGAAA TTAATCTGA ATAAATAATT CTTTCTGTTA 2128
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC 2178
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228
 GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328
 GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378
 AACTCCATT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC 2428

AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT
GGG

2478
2528
2531



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

[illegible]

- (2) INFORMATION FOR SEQUENCE ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2226 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-5 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAACAGAC ACTGAGGCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCCCTG AGAATCAGCC TCTGCTTGCT TGTGTACCCCT GAGGTGCCCT 400
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 684
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 728
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896
 TGG CTG ACT TGA 908
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1008
 CTTTCGGCAA GCCTCCGAGT CCTTGCACTT GGTCTTTGGC ATTGACGTGA 1058
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108
 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCAAAGACGG 1158
 GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC 1208
 CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG 1258
 GAGGGAGCAC AGTGTCTGTG GGGAGCCAG GAAGCTGCTC ACCCAAGATT 1308
 TGGTGCAGGA AAATACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC 1358
 ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA 1408
 CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC 1458
 CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG 1508
 CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG 1558
 CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC 1608
 TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT 1658
 TGGATGACTT TGAGATTTGT CTTTGTTCCT TTTTGAATT GTTCAAATGT 1708
 TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA 1758
 CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGCTTTGT 1808
 TTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT 1858
 TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC 1908
 TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC 1958
 TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCTTGGC 2008
 TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT 2058
 TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC 2108
 CCTGGGTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA 2158
 CAGGGTAGTA AAGCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT 2208
 GCCCTCTAAG ATGTAGAG 2226

- (2) INFORMATION FOR SEQUENCE ID NO: 17:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2305 base pairs
- (B) TYPE: nucleic acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-51 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTC ACCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAACAGAC ACTGAGGCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCTGTC AGAATCAGCC TCTGCTTGCT TGTGTACCTT GAGGTGCCCT 400
 CTCACCTTTT CTTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGS TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686
 GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC 728
 AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT 770
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 812
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 854
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 896
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 938
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 980
 TGG CTG ACT TGA 992
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA 1042
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1092
 CTTCCGGCAA GCCTCCGAGT CTTGTCAGCT GGTCTTTGGC ATTGACGTGA 1142
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTAC CTGCCTGGGA 1192
 CTCCTATGAT GGCTGTTGG TTTAATCAGA TCATGCCCA GACGGGCCTC 1242
 CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA 1292
 GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG 1342
 AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTGTTG 1392
 CAGGAAAATC ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC 1442
 TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG 1492
 CACGTGGTCA GGTCAATGC AAGAGTTCTC ATTTCTACC CATCCCTGCA 1542
 TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG 1592
 CCAGGGCCAC TGCAGGGGGG GCTGGGCCAG TGCACCTTC AGGGCTCCGT 1642
 CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCATT CTCTCTCTT 1692
 TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTCCTGTT CTATTGGATG 1742
 ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTT 1792
 TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG 1842
 TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA 1892
 TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC 1942
 AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAATGATGA 1992
 GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATT 2042
 GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTC TTGGCTTCTT 2092
 TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT 2142
 GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG 2192
 GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG 2242
 TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT 2292
 CTAAGATGTA GAG 2305

- (2) INFORMATION FOR SEQUENCE ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-6 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210
TGT GCC CCT GAG GAG 225

- (2) INFORMATION FOR SEQUENCE ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1947 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGAATCCAGA 50
 GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC 100
 TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCTCCTT CAGGTTCTCA 150
 GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC 200
 ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT 250
 GGTTACAAA TGAGGCCCCC CACAAGCTCC TTCTCTCCCC AGATCTGTGG 300
 GTTCTCCCC ATCGCCAGC TGCTGCCCCG ACTCCAGCCT GCTGCCCTGA 350
 CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG 400
 GATGCCTTGA GSCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG 450
 GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC CCTCTCTTCA CTCGTATTGA 500
 AGCCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCCTGA 550
 GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA 600
 GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC 650
 TAGACACACC CCGCTCACCT GCGTCCTTG TTCCA 685
 ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT 727
 ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA 769
 GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT 811
 GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC 853
 ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA 895
 CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC 937
 AGA GCA TGC CCG AGA CCG GCC TTC TGA 964
 TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG 1014
 GCAATCTGCG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT 1064
 TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC 1114
 TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT 1164
 CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG 1214
 AGTATGCAGC CAGGCTCAGT ACTAAAGAGA GCATTTCTTA CCCATCCCTG 1264
 CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC 1314
 AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTT 1364
 CACACATCCA CCACCTTCCC TGTCTGTGTA CATGAGGCCC ATTCTTCACT 1414
 CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG 1464
 GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC 1514
 GATTTGGAGG TTTATCTTTG TTTCTTTTGT CAGTCGTTCA AATGTTCTTT 1564
 TTAATGGATG GTGTAATGAA CTTCAACATT CATTTTCATGT ATGACAGTAG 1614
 GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT 1664
 TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG 1714
 CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAATAATGG 1764
 GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG 1814
 CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA 1864
 GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA 1914
 AATACAAAAC TTAGCCGGGC GTGGTGCGCG GTG 1947

- (2) INFORMATION FOR SEQUENCE ID NO: 20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1810 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-8 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA 50
 TCACAGAGCA TAAGAGGCCG AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT 100
 GTTTCCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA 150
 ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCACTCC TGGAGCCTTG 200
 GCCTTTGCCA GGAGGCTGCA CCTGAGATG CCCTCTCAAT TTCTCCTTCA 250
 GGTTTCGAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCG CAGAGAAGCA 300
 CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA 350
 CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT 400
 CAATTGCCCA GCTCCGGGCC AACTCTCTCT GCTGCCCTGA CCTGAGTCAT 450
 C 451
 ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA 493
 GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG 535
 CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC 577
 TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT 619
 GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT 661
 TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT 703
 GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC 745
 CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT 787
 GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA 829
 TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG 871
 AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC 913
 AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT 955
 GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC 997
 ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT 1039
 CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC 1081
 ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC 1123
 TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA 1156
 TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG 1206
 AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT 1256
 CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG 1306
 CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCATGCA AGAGTTCGCA 1356
 TTTCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT 1406
 TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG 1456
 GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCCT GCTCTGTTAC 1506
 ATGAGSCCCC TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA 1556
 GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC 1606
 AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG 1656
 AATTGTCCA ATGTTCTTTC TAATGGATGG TGTAATGAAC TTCAACATTC 1706
 ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA 1756
 GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA 1806
 ATTC 1810

- (2) INFORMATION FOR SEQUENCE ID NO: 21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1412 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-9 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG TGTCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC 50
 AGCAGTGAA3 GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT 100
 GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG 150
 TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC 200
 TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA 250
 GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT 300
 TGTTAGAACC TCCAAGGTTT GGTCTCAGC TGAAGTCTCT CACACACTCC 350
 CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC 400
 CTGACTGCTG CCCTGACCAG AGTCATC 427
 ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA 469
 GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA 511
 CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT 553
 GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT 595
 CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC 637
 GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC 679
 AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT 721
 CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG 763
 GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG 805
 GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA 847
 AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC 889
 GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG 931
 GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC 973
 CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC 1015
 AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC 1057
 AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG 1099
 AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC 1141
 GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA 1183
 AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG 1225
 CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC 1267
 AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA 1309
 AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG 1351
 GGA GAG GAG CAA GAG GGA GTC TGA 1375
 GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA 1412

- (2) INFORMATION FOR SEQUENCE ID NO: 22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 920 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-10 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCAGTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459
TCC ACC AGC	TCC TCT TTT	CCA TCC TCT	TTT CCC TCC	TCC TCC	501
TCT TCC TCC	TCC TCC TGC	TAT CCT CTA	ATA CCA AGC	ACC	543
CCA GAG GAG	GTT TCT GCT	GAT GAT GAG	ACA CCA AAT	CCT CCC	585
CAG AGT GCT	CAG ATA GCC	TGC TCC CCC	TCG GTC GTT	GCT	627
TCC CTT CCA	TTA GAT CAA	TCT GAT GAG	GGC TCC AGC	AGC CAA	669
AAG GAG GAG	AGT CCA AGC	ACC CTA CAG	GTC CTG CCA	GAC AGT	711
GAG TCT TTA	CCC AGA AGT	GAG ATA GAT	GAA AAG GTG	ACT GAT	753
TTG GTG CAG	TTT CTG CTC	TTC AAG TAT	CAA ATG AAG	GAG CCG	795
ATC ACA AAG	GCA GAA ATA	CTG GAG AGT	GTC ATA AAA	AAT TAT	837
GAA GAC CAC	TTC CCT TTG	TTG TTT AGT	GAA GCC TCC	GAG TGC	879
ATG CTG CTG	GTC TTT GGC	ATT GAT GTA	AAG GAA GTG	GAT CC	920

- (2) INFORMATION FOR SEQUENCE ID NO: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-11 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT 50
 CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT 100
 CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG 150
 GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG 200
 AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG 250
 CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC 300
 AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC 350
 ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC 400
 TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC 450
 TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG 500
 CCTGACCTGA TAGACCTGA GTCTTTTCC CAAGATATAC TACATGACAA 550
 GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT 600
 GATCACAAG GCAGAA 616
 ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT 658
 GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT 700
 GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT 742
 GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG 784
 TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA 826
 GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA 868
 GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT 910
 GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT 952
 ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG 994
 GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT 1036
 CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG 1078
 TAC ATA GCC AAT GCC AAT GGG AGG GAT CC 1107

- (2) INFORMATION FOR SEQUENCE ID NO: 24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2150 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: smage-I
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT 50
 CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC 100
 ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC 150
 TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT 200
 GCCCTTGAT GCAGGCCTAA GTTTTCTGT CTGCTTAACC CCTCCAAGTG 250
 AAGCTAGTGA AAGATCTAAC CCACCTTTGG AAGTCTGAAA CTAGACTTTT 300
 ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG 350
 AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCCTAG AAAG 394
 ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT 436
 CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT 478
 TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT 520
 ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG 565
 AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG 604
 GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT 646
 TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT 688
 TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA 730
 GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT 772
 GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA 814
 GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG 856
 AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG 898
 ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT 940
 AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA 982
 ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG 1024
 GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA 1066
 CTG GST CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG 1108
 TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC 1150
 TTC ATG AAG GST AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA 1192
 TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG 1234
 ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG 1276
 GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC 1314
 CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA 1360
 ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT 1402
 GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT 1444
 CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA 1486
 GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT 1528
 AAC ATG TAG 1537
 TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG 1587
 AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCTGTAT 1637
 ACATTAGTAG AATGGAGGCT ATTTTGTGTA CTTTCAAAT GTTTGTTAA 1687
 CTAACAGTG CTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC 1737
 TGTCATTGT CAGATTAGGA CTGTGTTTGT TATTGCAAC AAAGTGGAAA 1787
 ACATTATTTT GTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG 1837
 GATTGTGATG GCAATGTGAT ATCATAAGT GGTGAAACAA CAGTGAAGTG 1887
 GGAAAGTTA TATTGTTAAT TTTGAAATTT TTATGAGTGT GATTGCTGTA 1937
 TACTTTTTTC TTTTGTGAT AATGCTAAGT GAAATAAAGT TGGATTGAT 1987
 GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA 2037
 TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA 2087
 GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA 2137
 GTTATCAGAG TCT 2150

- (2) INFORMATION FOR SEQUENCE ID NO: 25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2099 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: smage-II
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:



ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACCTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCTTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGSTATCTCT	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCCTG	CAGAGGAAGC	650
AGSGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTTCAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAAACAAGAA	TATAAGGAGC	AATTCCTCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCAGC	1050
ACTCATTCTT	ATTTGCTGGT	AGGCAAACCTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AAGTGGGGGT	TGCCTAGGAC	AGGCTCCTTA	ATGCTGTCTC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AGGGGTGTTT	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTGTTT	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAACCTG	1750
TCACTTGTC	GATTAGGACT	TGTTTTGTTA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTCTTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACTCTA	TTACTTTATT	2050
ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

- (2) INFORMATION FOR SEQUENCE ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acids
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
5

Done.